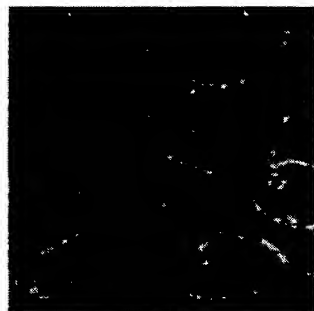
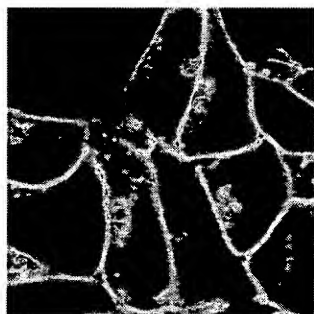


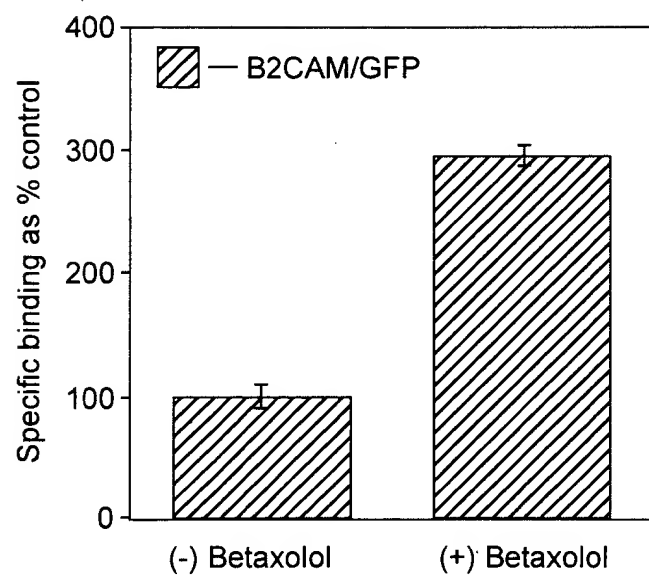
FIG. 3



(-) Betaxolol



(+) Betaxolol



# REPLACEMENT SHEET

FIG. 6B

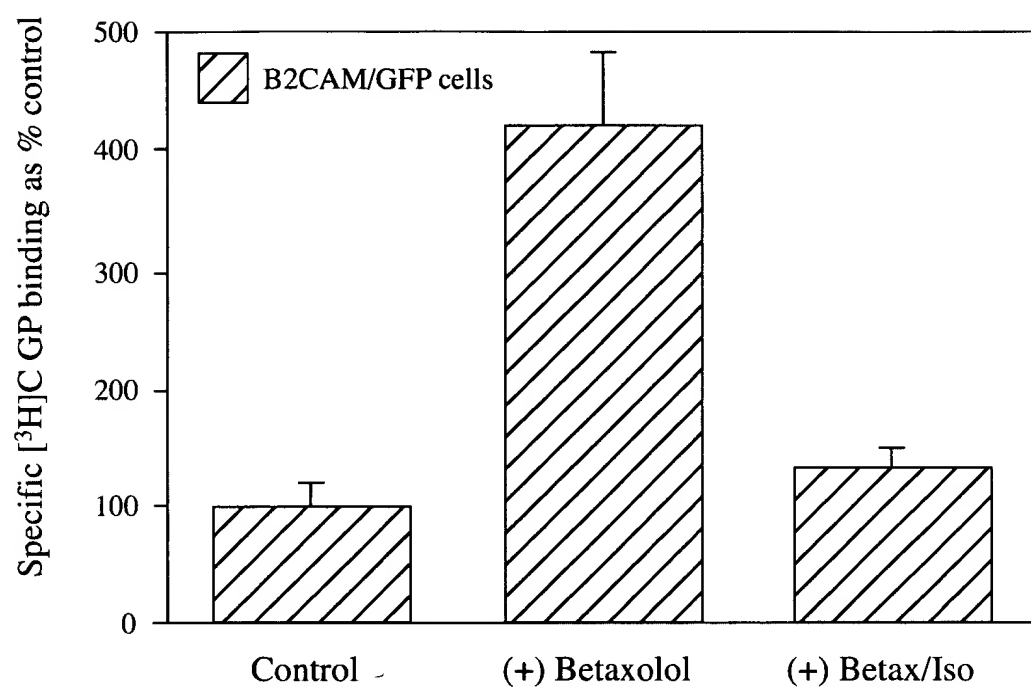
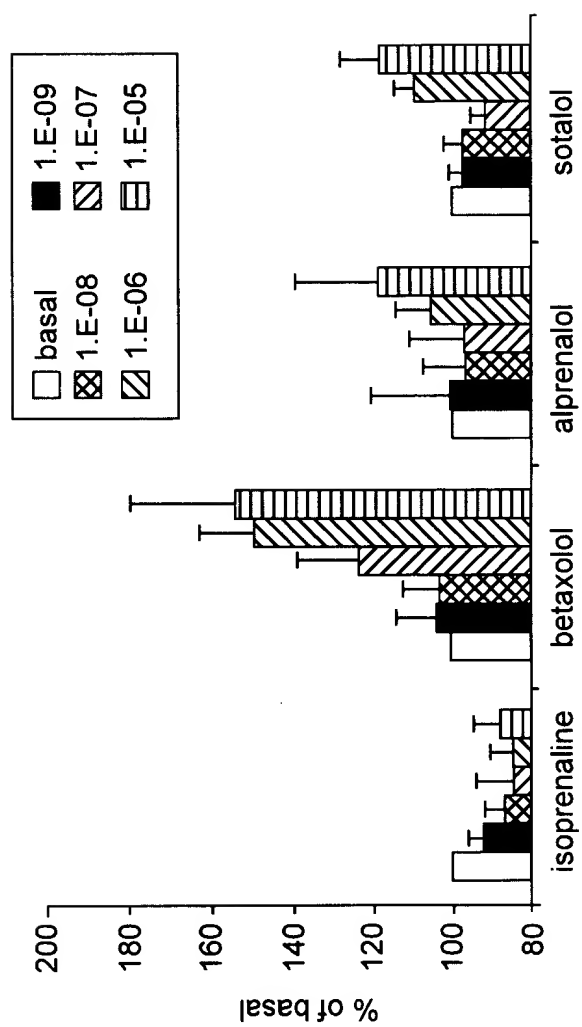
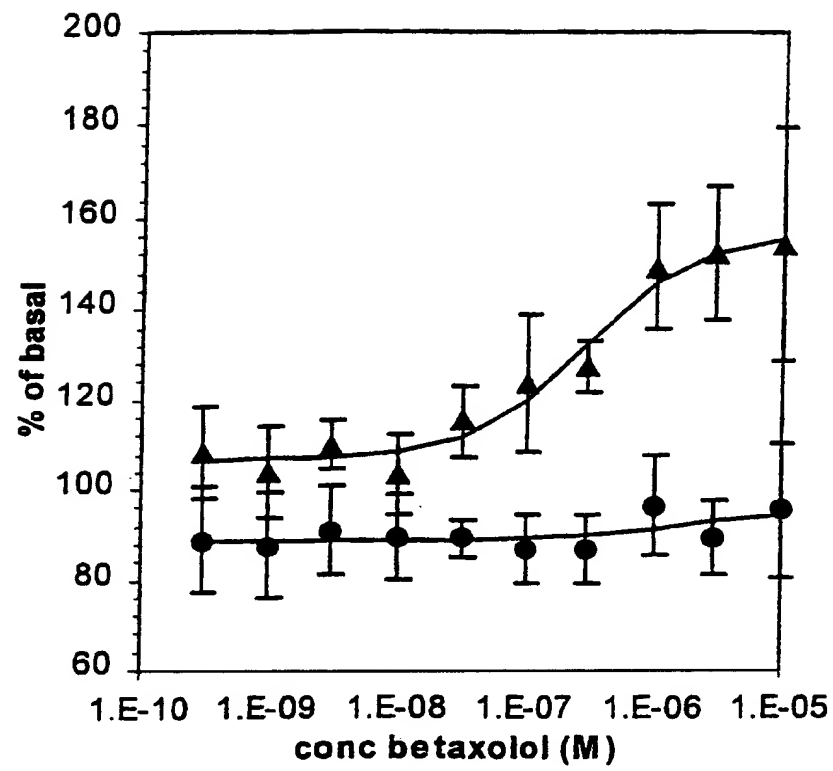


FIG.7A



REPLACEMENT SHEET

FIG. 7B



REPLACEMENT SHEET

FIG. 7C

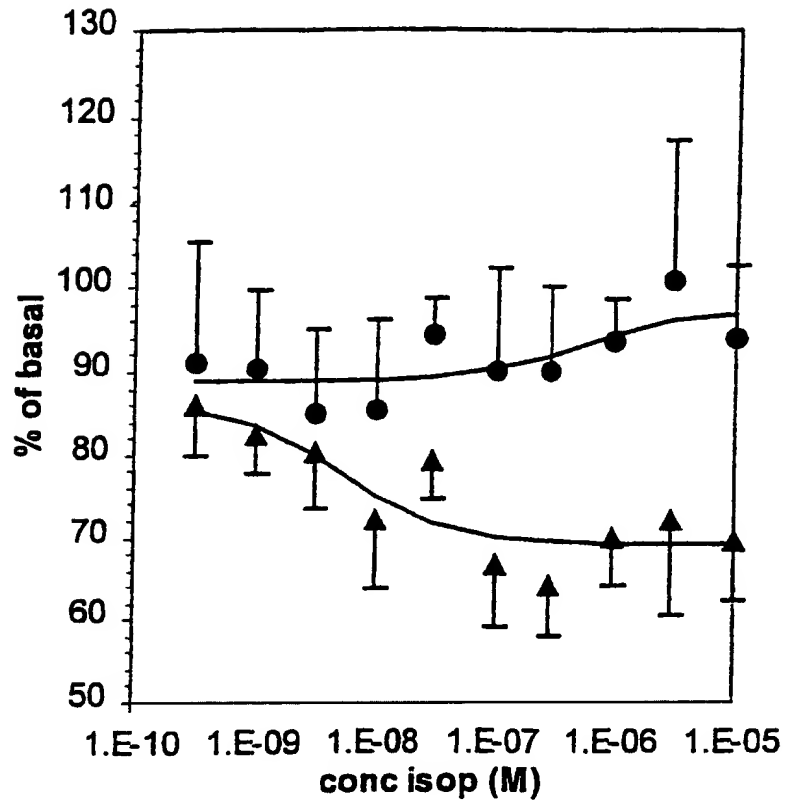
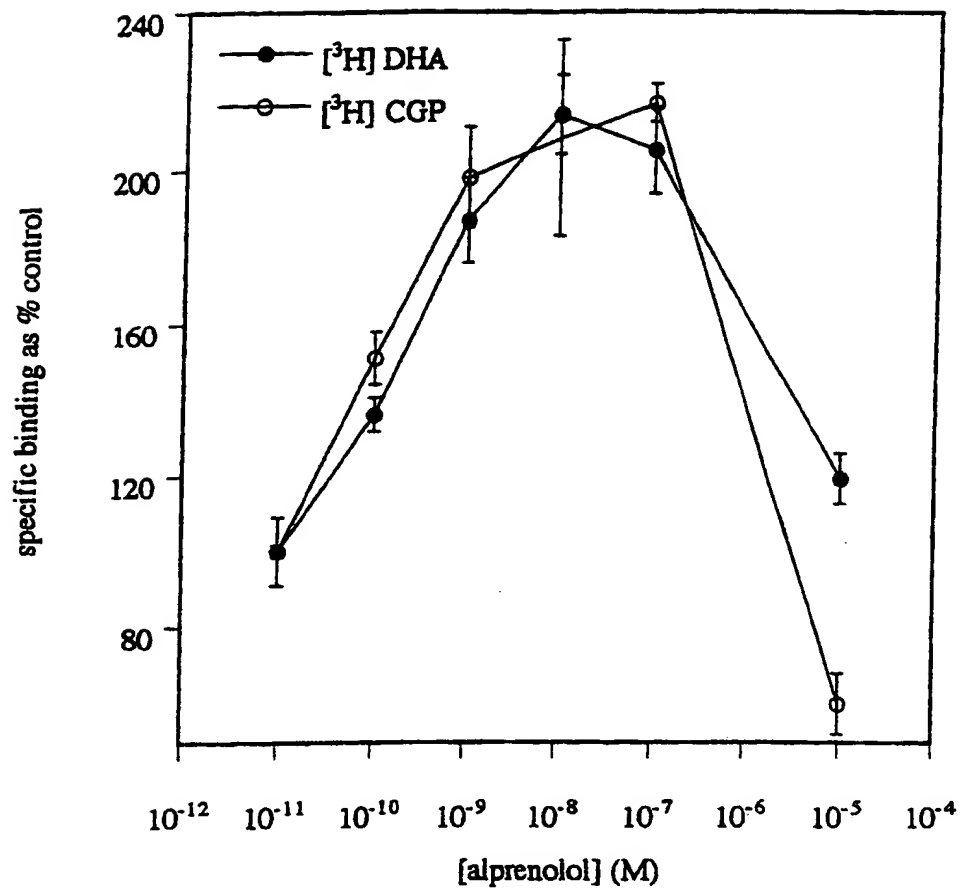


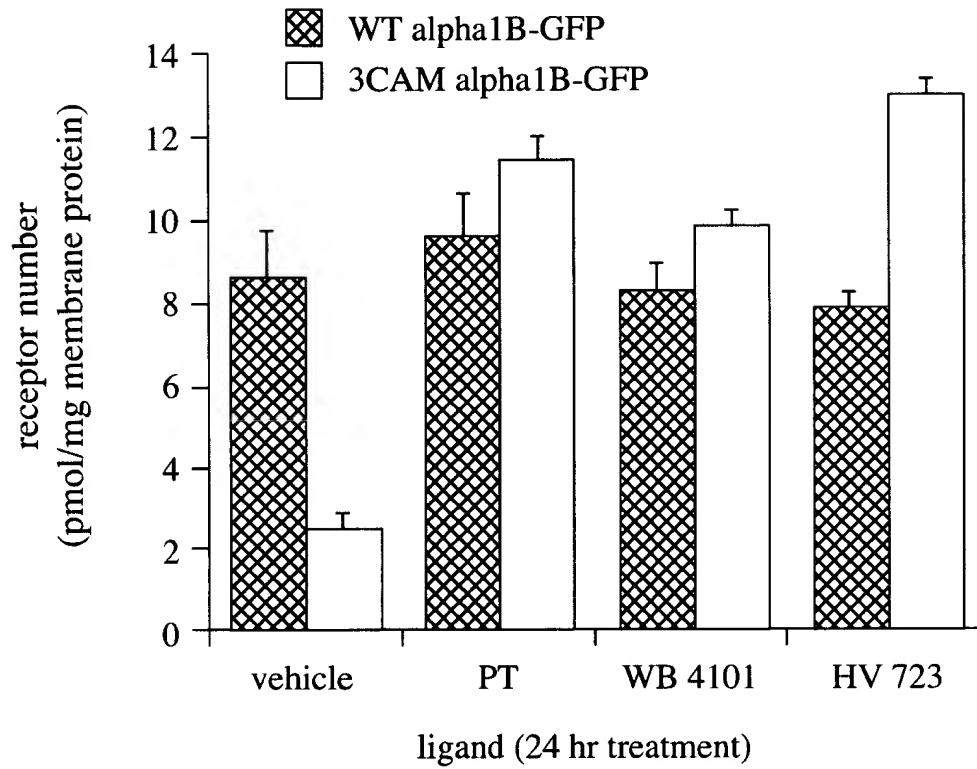
FIG. 8A



The schematic diagram illustrates the protein structure of the A293L, K290H, and R288K variants. The protein sequence is shown from the N-terminus (NH<sub>2</sub>) to the C-terminus (COOH). Specific residues are highlighted in black circles, indicating the locations of the mutations. The residues are numbered at 142, 293, 290, and 288. A legend indicates that black circles represent the A293L, K290H, and R288K mutations.

A293L  
K290H  
R288K

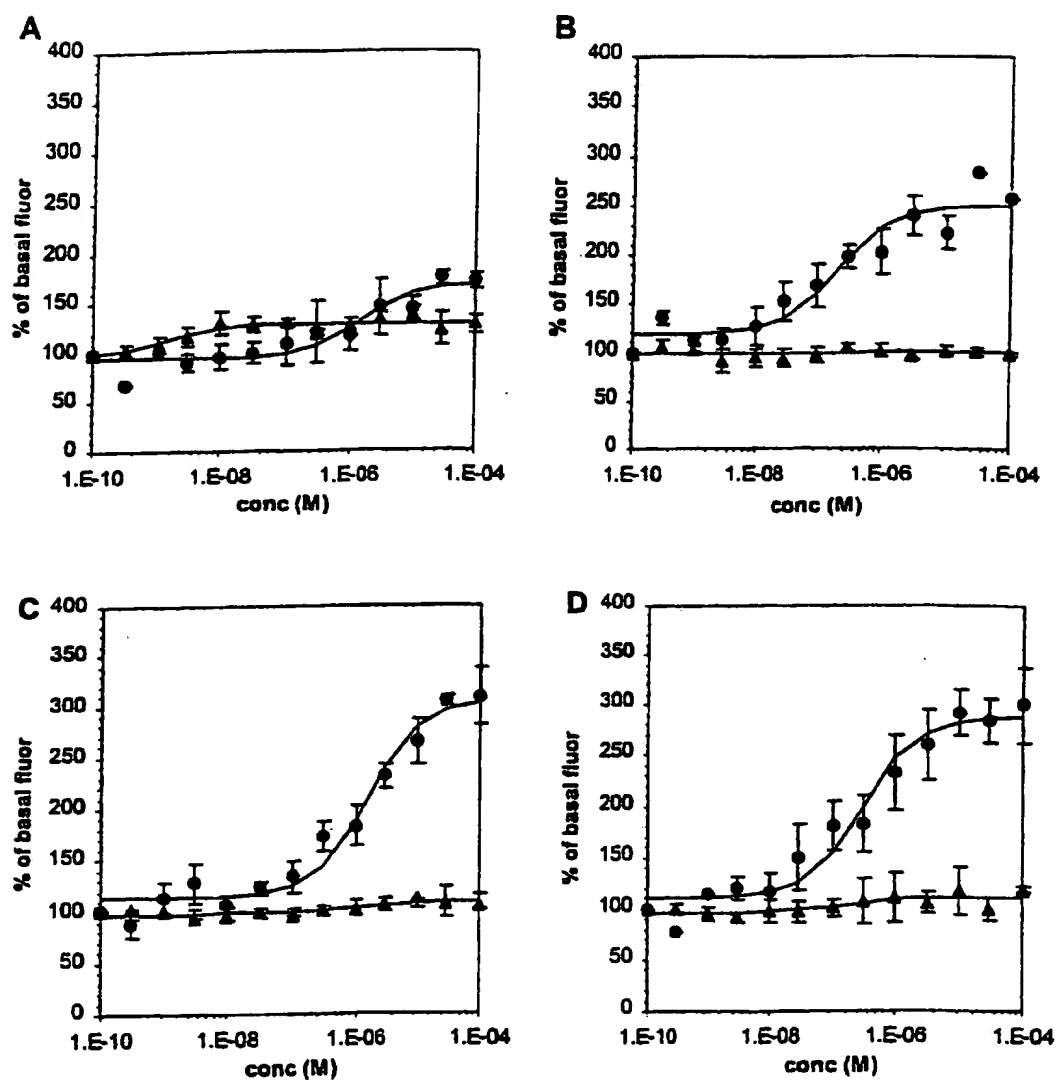
FIG. 10C





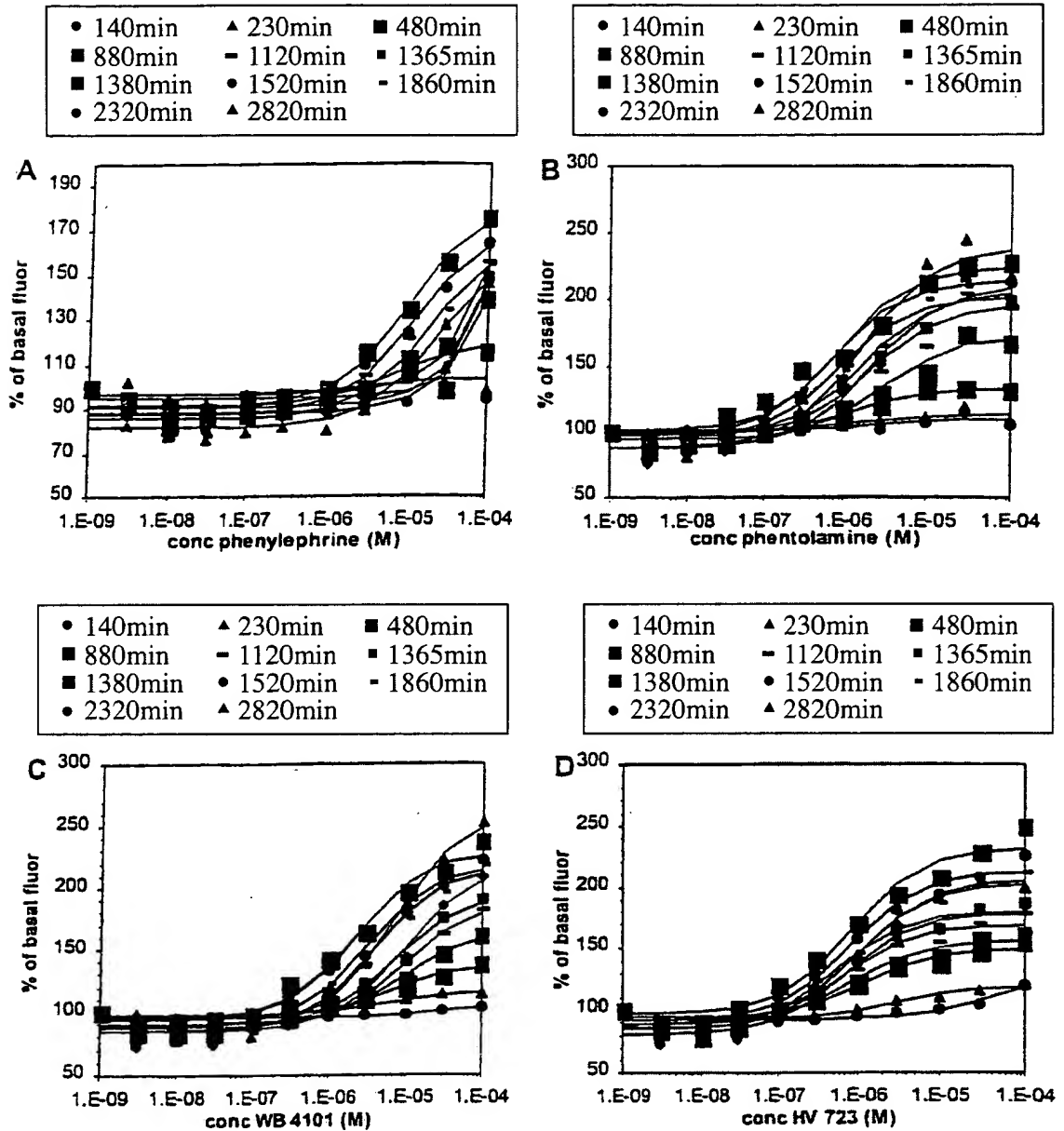
# REPLACEMENT SHEET

FIG. 11



# REPLACEMENT SHEET

FIG. 12



# REPLACEMENT SHEET

FIG. 13

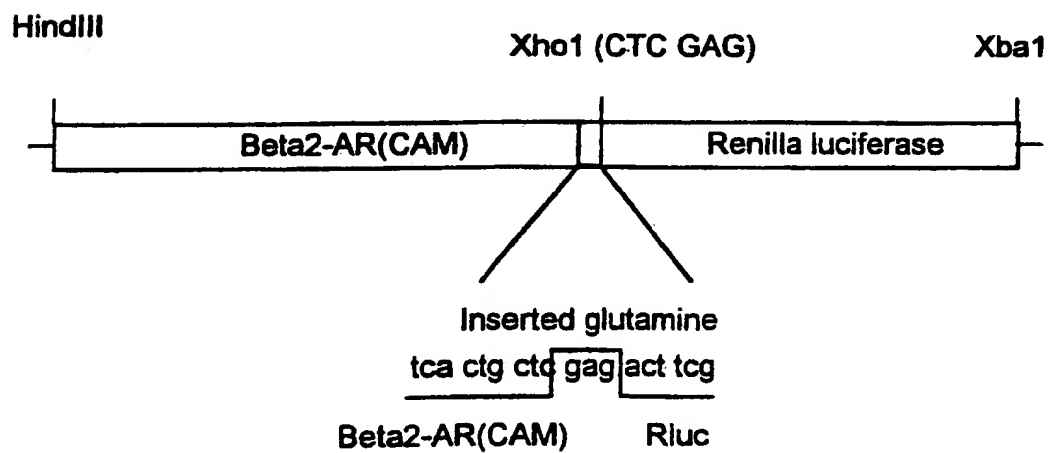
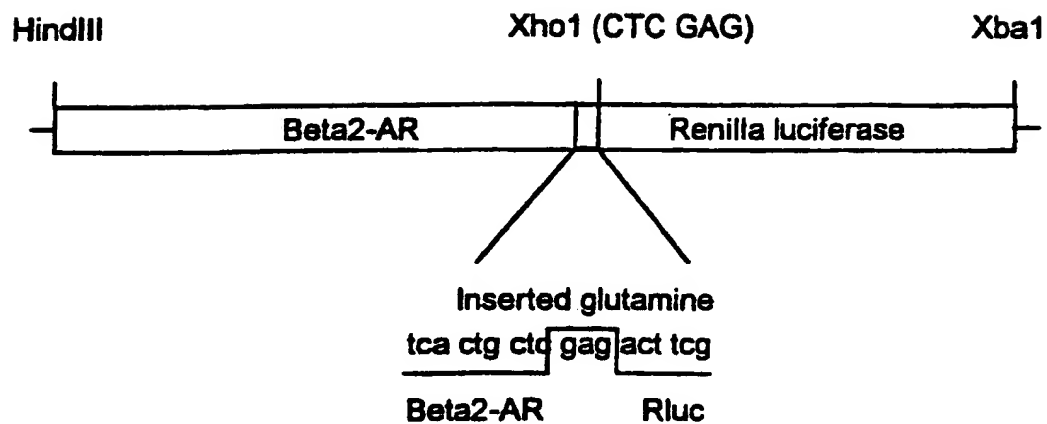
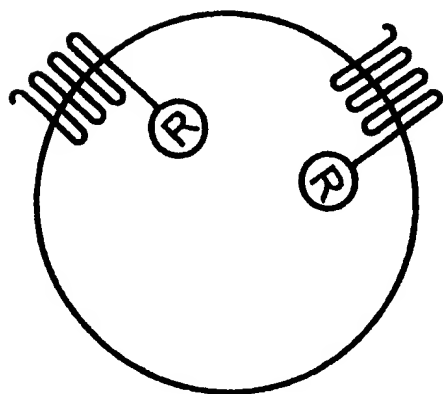


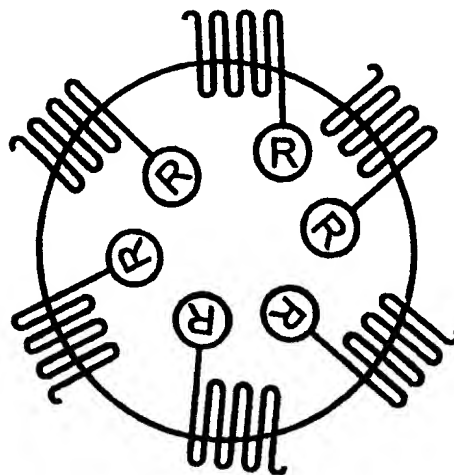
FIG. 14

CAM $\beta_2$ AR	Renilla Luciferase
------------------	--------------------

(-) Antagonist



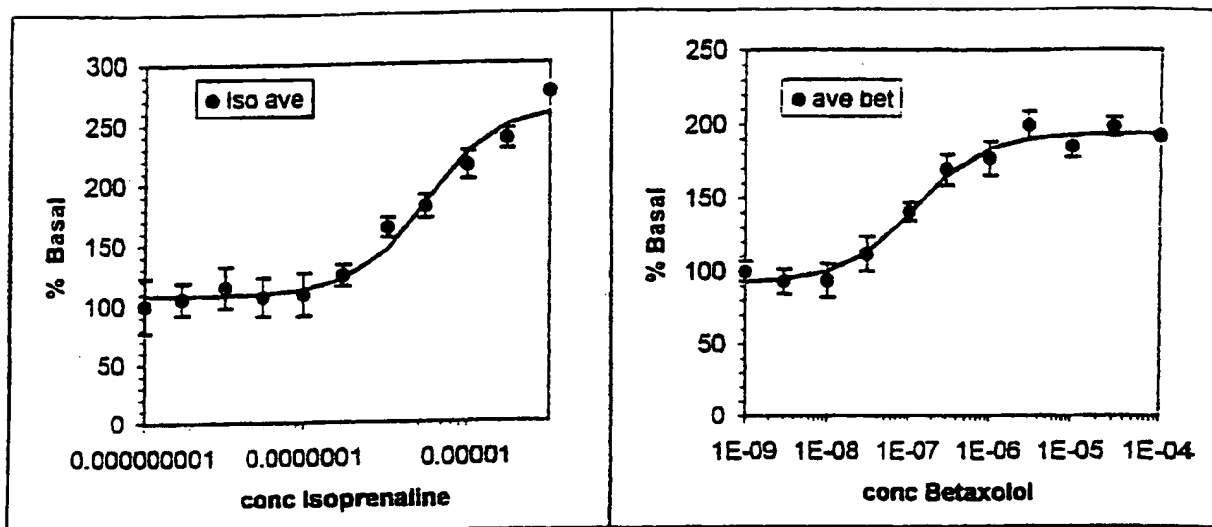
(+) Antagonist



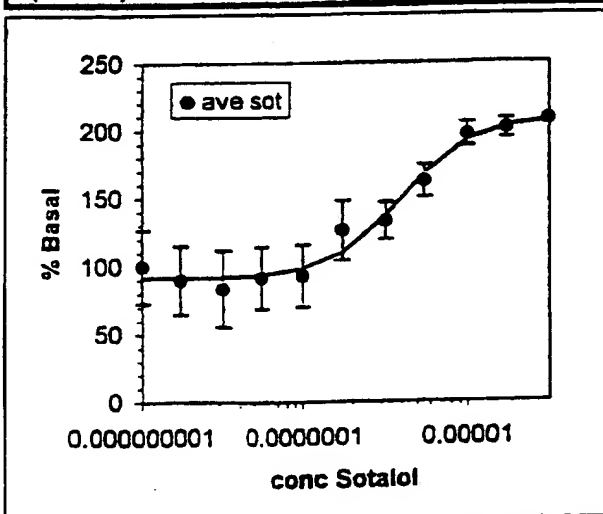
Upregulation monitored by increased  
luciferase activity in cells

# REPLACEMENT SHEET

FIG. 15



Paramete	Value	SE	Lower CL	Upper CL	Paramete	Value	SE	Lower CL	Upper CL
a (iso ave)	107.98	4.99006	96.4729	119.4871	a (ave bet)	91.99781	4.066952	82.6194	101.3762
c (iso ave)	3.04E-06	8.74E-07	1.57E-06	5.9E-06	c (ave bet)	1.16E-07	2.64E-08	6.85E-08	1.96E-07
d (iso ave)	263.6671	9.532958	241.684	285.6501	d (ave bet)	194.6117	3.153874	187.3389	201.8846
b (iso ave)	1	0	1	1	b (ave bet)	1	0	1	1



Paramete	Value	SE	Lower CL	Upper CL
a (ave sot)	91.61328	3.703476	83.07304	100.1535
c (ave sot)	1.59E-06	4.07E-07	8.77E-07	2.87E-06
d (ave sot)	208.4677	5.759934	195.1852	221.7501
b (ave sot)	1	0	1	1

REPLACEMENT SHEET

FIG. 17

